

FIG.. 1A

34 total
sheets

FIG.-1B - 1

50	Ala	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Asn	60	Asp																	
549	GCA	GCC	GGG	GCA	GCC	AGC	ATG	GTC	CCT	TCT	GTG	ATG	GTC	AAT	CCT	TTC	CAA	GCA	AAC	AAC	TCT	CAC	GGA	ACT	CAC	GTT	GCC						
70	Gly	Thr	Val	Ala	Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Phe	Gln	Asp	Asn	Ser	His	Gly	Thr	His	Val	Ala						
824	GGC	ACA	GTC	GTT	GGG	GCT	CCT	AAT	AAC	TCA	ATC	GGT	GAC	GCT	TCA	ATA	GCA	ATA	GAA	TCA	AGC	AAC	AAC	TCT	CAC	GGA	ACT	CAC	GTT	GCC			
100	Asp	Ala	Asp	Ala	Asp	Gly	Ser	Gly	Gly	Tyr	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Leu	Leu	Asn	Ser	Ala	Asn	Asn	Ala	Val	Lys			
659	GTT	CTC	GGT	GCT	GAC	GGT	TCC	GGC	CAA	TAC	AGC	TGG	ATC	ATT	AAC	GGA	ATC	GAG	TGC	GGC	ATC	GCA	AAC	AAT	ATG								
120	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Ala	Leu	Lys	Ala	Ala	Val	Asp	Lys	Ala	Val	Ala	Asn	Met						
774	GAC	GTT	ATT	AAC	ATG	AGC	CTC	GGC	GGG	CCT	TCT	GCT	TCT	GCT	GCT	TTA	AAA	GCG	GCA	GTT	GAT	AAA	GCC	GTT	GCA	AGC	TCA	AGC	ACA	GTC			
130	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Ala	Leu	Lys	Ala	Ala	Val	Asp	Lys	Ala	Val	Ala	Asn	Met						
140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450		
849	TCC	GGC	GTC	GTA	GTC	GTT	GGC	GCA	GCC	GGT	AAC	GAA	GGC	ACT	TCC	GGC	AGC	TCA	AGC	ACA	GTC	GGC	TAC	CCT	GGT								
924	AAA	TAC	CCT	TCT	GTC	ATT	GCA	GTA	GGC	GCT	GTT	GAC	AGC	AGC	AAC	CAA	AGA	GCA	TCT	TTC	TCA	AGC	GTA	GGG	GGT								
999	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Pro	Gly	Asn	Lys	Trp	Gly	Ala	Trp	Asn	Gly								
1074	ACG	TCA	ATG	GCA	TCT	CCC	GAC	GCT	GGC	GGG	GCT	GGT	TTG	ATT	CCT	TCT	AAG	CAC	CCC	AAC	TCT	AAG	TGG	ACA	AAC	ACT							

FIG.-1B - 2

Gln Val Arg Ser Ser 250 Gln
Glu Asn Thr Thr Lys Leu Gly Asp Ser 260 Phe Tyr Tyr Gly Lys Gly Leu Ile Asn
1149 CAA GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA CTT GAT GGT TAC TCT TAC TAT GGA AAA GGG CTG ATC AAC

270 275 TERM

Val Gln Ala Ala Glu DC

1224 GTA CAG GCG GCA GCT CAG TAA AACATAAAACCCGGCTTGCCCCGGGTTTTATTTCCTCCGCATGTCAATCGCTCC

1316 ATAAATCGACGGATGGCTCCCTCTGAAATAACCGAGAACGGGAAACGGGCTAACCGGGCTAACGCCAACGTCCTGAACCGTCTCAATGCCCG

1416 CTTCGGGTTCCGGTCAGCTCAATGCCGTAAACGGTCCGGGCTTCCCTGATACCGGGAAACGGCATTCGTAAATCGGTCA

FIG.- 1B - 3

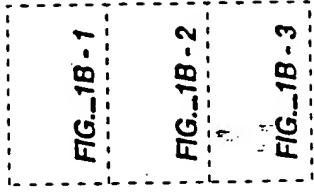


FIG.- 1B

CONSERVED RESIDUES IN SUBTILISINS FROM
BACILLUS AMYLOLIQUEFACIENS

1	10	20
A Q S V P . G	A P A . H . . .	G
21	30	40
. T G S . V K V A V . D . G	H P	
41	50	60
D L . . . G G A S . V P	Q D	
61	70	80
. N . H G T H V A G T . A A L N N S I G		
81	90	100
V L G V A P S A . L Y A V K V L G A . G		
101	110	120
S G . . S . L . . G . E W A . N		
121	130	140
V . N . S L G . P S . S A . .		
141	150	160
. G V . V V A A . G N . G . . .		
161	170	180
. Y P . . Y A V G A .		
181	190	200
D . . N . . A S F S . . G . . L D . . A		
201	210	220
P G V . . Q S T . P G . . Y . . . N G T		
221	230	240
S M A . P H V A G A A A L . . . K . . .		
241	250	260
W . . . Q . R . . L . N T . . . L G . . .		
261	270	
. . Y G . G L . N . . A A . . .		

FIG.-2

COMPARISON OF SUBTILISIN SEQUENCES FROM:

G. amylolyticus

B. STUDIES

B. licheniformis

B. licheniformis
B. lensus

01 A Q S V P Y G V S Q I K A P A L H . S Q G Y T G S N V K V A V I D S S H P
 10 A Q S V P Y G I S Q I K A P A L H . S Q G Y T G S N V K V A V I D S S H P
 20 A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V I D S S H P
 30 A Q S V P W G I S R V Q A P A H N R G L T G S G V K V A V I D S S H P
 * A Q S V P W G I S R V Q A P A H N R G L T G S G V K V A V I D S S H P

41 DLK VAGGASHV PSETNPP QDNN SHGTHVAGTVA
 50 DLNVRGGASSPV PSETNPYQDGSSHGTTIA
 60 DLNVVGGASSPV AGEAYN*T DGNCHGTTVA
 70 DLNIRGGASSPV PGE* PSTQDGNCHGTTIA
 ALNNSIG ALNNSIG ALNNSIG ALDNNTG
 ALNNSIG ALNNSIG ALNNSIG ALNNSIG

81	V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D
82	V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S H N M D
83	V L G V A P S V S L Y A V K V L N S S G S C S Y S G I V S G I E W A T T N G M D
84	V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N N G M H
85	V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D

121	VIN	M	S	L	G	G	P	S	G	SA	A	K	A	V	D	K	A	V	A	S	G	V	V	V	V	A	G	N	E	C	T	S	G						
	I	N	M	S	L	G	G	P	T	G	S	T	A	L	K	T	V	V	D	K	A	V	S	G	I	V	V	V	A	A	G	N	E	G	S	G			
	V	I	N	M	S	L	G	G	A	S	G	S	T	A	M	K	Q	V	D	N	A	Y	A	R	G	V	V	V	V	A	A	G	N	S	G	N	S	G	
	V	A	N	L	S	L	G	S	P	S	P	S	A	T	L	E	Q	A	V	N	S	A	T	S	R	G	V	L	V	V	A	S	G	N	S	G	A	S	G

FIG. 3A

દ્વારા પ્રદાન કરેલું હોય અને એટા સ્પેચ માટે એક વિશેષ પ્રદાન કરેલું હોય

161	170	180	190
SSSTVGYPPCKYPSVIAVGAVDSSNQRASFPSSVGPELDVMA	SSTVGYPAKYPPSTIAVGAVNSSNQRASFPSSAGSELDVMA	SNTIGYPAKYDSSVIAVGAVDSNSNRASFPSSVGAELEVMA	
* * * ISYPARYANAMAVGATDQNRRASFSQYGAQLDIVA			
201	210	220	230
PGVSIQOSTLPGNKYGAINGTSMASPHVAGAAALILSKHPPN	PGVSIQOSTLPGGTYGAYNGTSMATPHVAGAAALILSKHPT	PGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPPN	
PGVNQQSYTPGSTYASLNGTSMATPHVAGAAALVKQNNPS			
241	250	260	270
WTNTQVRSSLENNTKLGDSFYXGKGLINVQAAAQ	WTNAQVRDRLESSNTYLGNSFYXGKGLINVQAAAQ	LSSASQVRNRLLNTATSYLGSSSTNLGYSGGLVNAEAATR	
WSNVQIRNHLKNTATSSLGSTMNL			

FIG._3B

FIG._3A

FIG._3

FIG._3B

FIG. 4

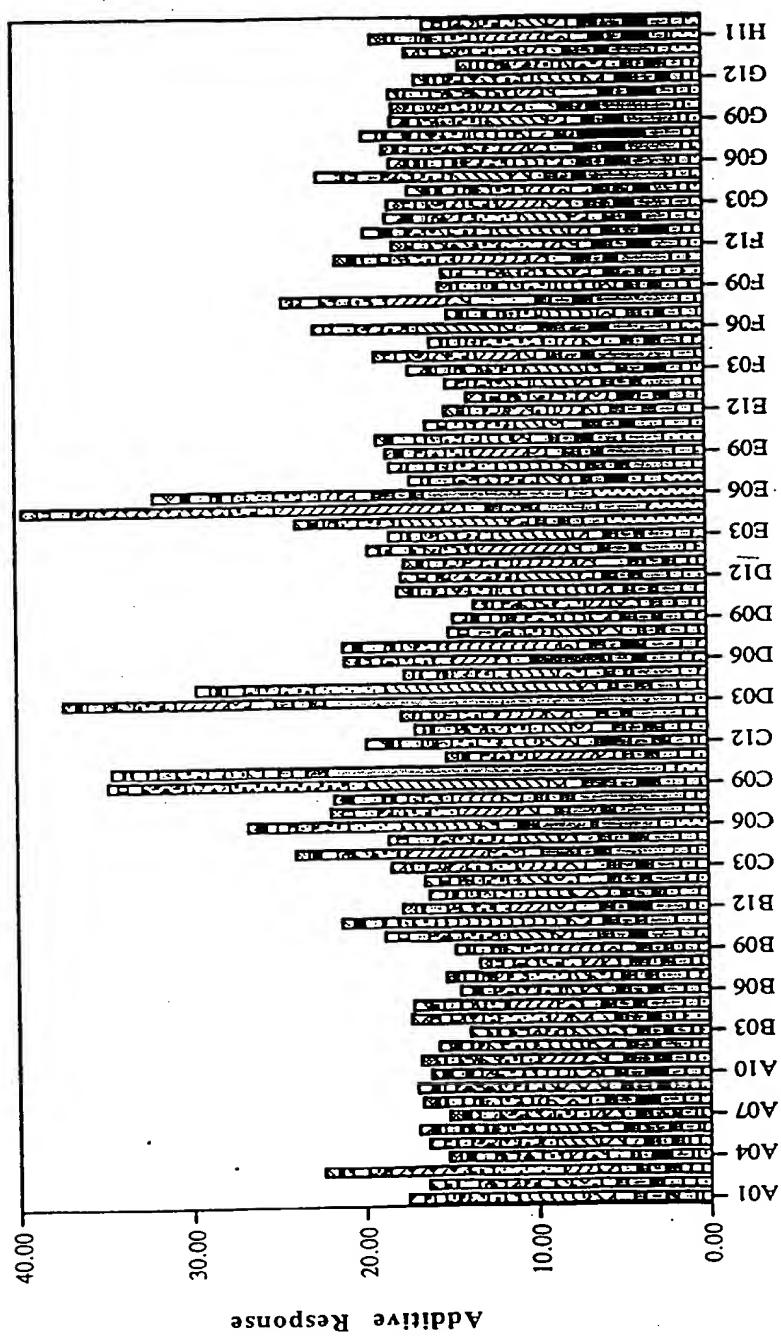
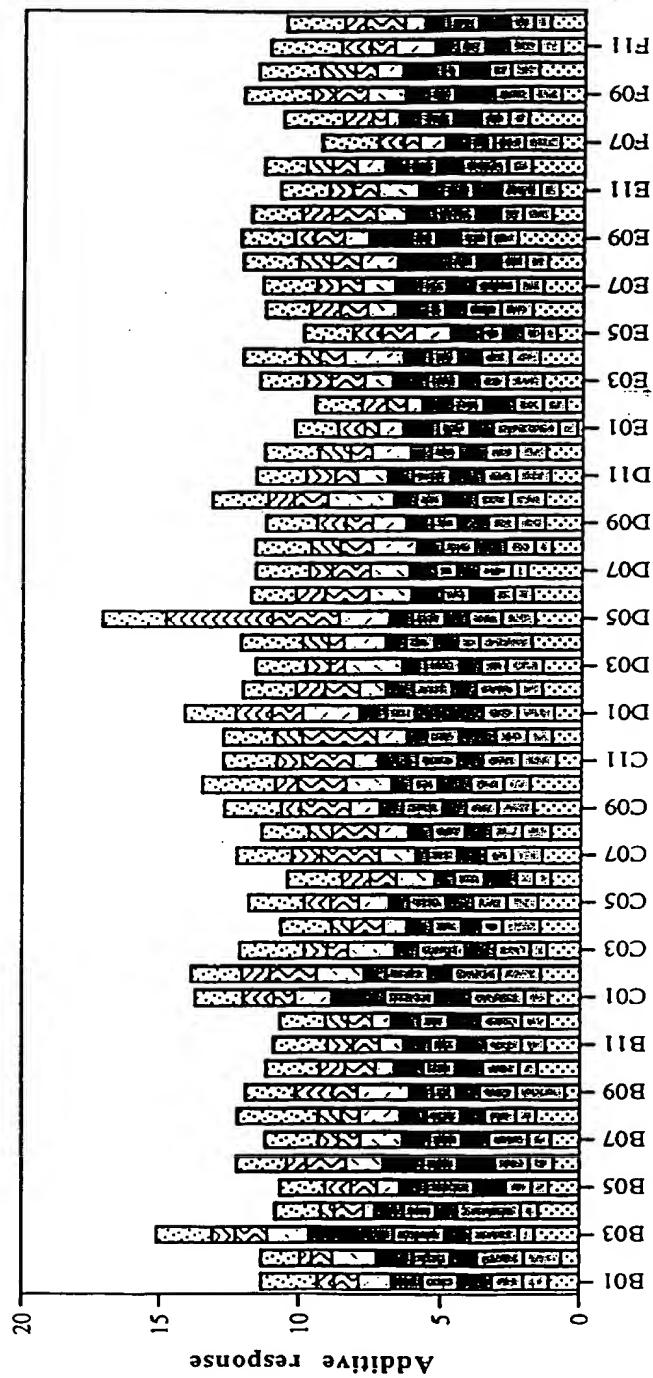


FIG. 5



1	A12	IKDFHVYFRESRDAG	49	E12	SATSRGVLVVAASGN
2	A11	LEQAVNSATSRGVLV	50	E11	SRGVLVVAASGNSGA
3	A10	AQSVPWGISRVQAPA	51	E10	VLVVAASGNSGAGSI
4	A9	VPWGISRQAPAAHN	52	E9	VAASGNSGAGSISYP
5	A8	GISRVQAPAAHNRLG	53	E8	SGNSGAGSISYPARY
6	A7	RVQAPAAHNRLTGS	54	E7	SGAGSISYPARYANA
7	A6	APAAHNRLTGSGVK	55	E6	GSISYPARYANAMAV
8	A5	AHNRLTGSGVKVAV	56	E5	SYPARYANAMAVGAT
9	A4	RGLTGSGVKVAVLDT	57	E4	ARYANAMAVGATDQN
10	A3	TGSGVKVAVLDTGIS	58	E3	ANAMAVGATDQNNNR
11	A2	GVKVAVLDTGISTHP	59	E2	MAVGATDQNNNRASF
12	A1	VAVLDTGISTHPDLN	60	E1	GATDQNNNRASFSQL
13	R12	LDTGISTHPDLNIRG	61	F12	DQNNNRASFSQLYAG
14	B11	GISTHPDLNIRGGAS	62	F11	NNRASFSQLYAGLDI
15	B10	THPDLNIRGGASFVP	63	F10	ASFSQYAGLDIVAP
16	B9	DLNIRGGASFVPGEP	64	F9	SQYAGLDIVAPGVN
17	B8	IRGGASFVPGEPSTQ	65	F8	GAGLDIVAPGVNVQS
18	B7	GASFVPGEPSTQDGN	66	F7	LDIVAPGVNVQSTYP
19	B6	FVPGEPESTQDGNGHG	67	F6	VAPGVNVQSTYPGST
20	B5	GEPSTQDGNGHGTIV	68	F5	GVNVQSTYPGSTYAS
21	B4	STQDGNGHGTIVAGT	69	F4	VQSTYPGSTYASLNG
22	B3	DGNHGHTIVAGTIAA	70	F3	TPGSTYASLNGTSM
23	B2	GHGHTIVAGTIAALNN	71	F2	GSTYASLNGTSMATP
24	B1	THVAGTIAALNNSIG	72	F1	YASLNGTSMATPHVA
25	C12	AGTIAALNNSIGVLG	73	G12	LNGTSMATPHVAGAA
26	C11	IAALNNSIGVLGVAP	74	G11	TSMATPHVAGAAALV
27	C10	LNNNSIGVLGVAPSAC	75	G10	ATPHVAGAAALVKQK
28	C9	S1GVLGVAPSACELYA	76	G9	HVAGAAALVKQKNPS
29	C8	VLGVAPSACELYAVKV	77	G8	GAAALVKQKNPSWSN
30	C7	VAPSACELYAVKLGA	78	G7	ALVKQKNPSWSNVQI
31	C6	SAELYAVKLGASGS	79	G6	KQKNPSWSNVQIRNH
32	C5	LYAVKLGASGSGSV	80	G5	NPSWSNVQIRNHLKN
33	C4	VKVLGASGSGSVSSI	81	G4	WSNVQIRNHLKNTAT
34	C3	LGASGSGSVSSIAQG	82	G3	VQIRNHLKNTATSLG
35	C2	SGSGSVSSIAQGLEW	83	G2	RNHLKNTATSLGSTN
36	C1	GSVSSIAQGLEWAGN	84	G1	LKNTATSLGSTNLYG
37	D12	SSIAQGLEWAGNNGM	85	H12	TATSLGSTNLYGSGL
38	D11	AQGLEWAGNNGMHVA	86	H11	SLGSTNLYGSGLVNA
39	D10	LEWAGNNGMHVA	87	H10	STNLYGSGLVNAEAA
40	D9	AGNNGMHNVA	88	H9	NLYGSGLVNAEAAATR
41	D8	NGMHVANLSLGSPSP			
42	D7	HVANLSLGSPSPSAT			
43	D6	NLSLGSPSPSATLEQ			
44	D5	LGSPSPSATLEQAVN			
45	D4	PSPSATLEQAVNSAT			
46	D3	SATLEQAVNSATS			
47	D2	LEQAVNSATS			
48	D1	AVNSATS			

FIG. 6A

1	A12	IKDFHVYFRESRDAG	49	E12	KKIDVLNLSIGGPDF
2	A11	DAELHIFRVFTNNQV	50	E11	DVLNLSIGGPDFMDH
3	A10	PLRRASLSLGSGFWH	51	E10	NLSIGGPDFMDHPFV
4	A9	RASLSLGSGFWHATG	52	E9	IGGPDFMDHPFVDKV
5	A8	LSLGSGFWHATGRHS	53	E8	PDFMDHPFVDKVWEL
6	A7	GSGFWHATGRHSSRR	54	E7	MDHPFVDKVWELTAN
7	A6	FWHATGRHSSRLLR	55	E6	PFVDKVWELTANNVI
8	A5	ATGRHSSRLLRAIP	56	E5	DKVWELTANNVIMVS
9	A4	RHSSRLLRAIPRQV	57	E4	WELTANNVIMVSAIG
10	A3	SRRLLRAIPRQVAQT	58	E3	TANNVIMVSAIGNDG
11	A2	LLRAIPRQVAQTLQA	59	E2	NVIMVSAIGNDGPLY
12	A1	AIPRQVAQTLQADVL	60	E1	MVSAIGNDGPLYGTJ
13	B12	RQVAQTLQADVLWQM	61	F12	AIGNDGPLYGTLNTP
14	B11	AQTLQADVLWQMGT	62	F11	NDGPLYGTLNTPADQ
15	B10	LQADVLWQMGTGAN	63	F10	PLYGTLNNPADQMDV
16	B9	DVLWQMGTGANVRV	64	F9	GTLNNPADQMDVIGV
17	B8	WQMGTGANVRVAVF	65	F8	NNPADQMDVIGVGGI
18	B7	GYTGANVRVAVFDTG	66	F7	ADQMDVIGVGGIDFE
19	B6	GANVRVAVFDGLSE	67	F6	MDVIGVGGIDFEDNI
20	B5	VRVAVFDGLSEKHP	68	F5	IGVGGIDFEDNIARF
21	B4	AVFDGLSEKHPFK	69	F4	GGIDFEDNIARFSSR
22	B3	DTGLSEKHPFKNVK	70	F3	DFEDNIARFSSRGMT
23	B2	LSEKHPFKNVKERT	71	F2	DNIARFSSRGMTTWE
24	B1	KHPFKNVKERTNWT	72	F1	ARFSSRGMTTWEPLG
25	C12	HFKNVKERTNWTNER	73	G12	SSRGMTTWEPLGGY
26	C11	NVKERTNWTNERTLD	74	G11	GMTTWEPLGGYGRMK
27	C10	ERTNWTNERTLDDGL	75	G10	TWEPLGGYGRMKPDI
28	C9	NWTNERTLDDGLGHG	76	G9	LPGGYGRMKPDIVTY
29	C8	NERLDDGLGHGTFV	77	G8	GYGRMKPDIVTYGAG
30	C7	TLDDGLGHGTFVAGV	78	G7	RMKPDIVTYGAGVRG
31	C6	DGLGHGTFVAGVIAS	79	G6	PDIVTYGAGVRGSGV
32	C5	GHGTFVAGVIASMRE	80	G5	VTYGAGVRGSGVKGG
33	C4	TFVAGVIASMRECQG	81	G4	GAGVRGSGVKGGCRA
34	C3	AGVIASMRECQGFAP	82	G3	VRGSGVKGGCRALSG
35	C2	IASMRECQGFAPDAE	83	G2	SGVKGGCRALSGTSV
36	C1	MRECQGFAPDAELHI	84	G1	KGGCRALSGTSVASP
37	D12	CQGFAPDAELHIFRV	85	H12	CRALSGTSVASPVVA
38	D11	FAPDAELHIFRVFTN	86	H11	LSGTSVASPVAGAV
39	D10	DAELHIFRVFTNNQV	87	H10	TSVASPVAGAVTLL
40	D9	LHIFRVFTNNQSYT	88	H9	ASPVAGAVTLLVST
41	D8	FRVFTNNQSYTSWF	89	H8	VVAGAVTLLVSTVQK
42	D7	FTNNQSYTSWFLDA	90	H7	GAVTLLVSTVQKREL
43	D6	NQVSYTSWFLDAFN	91	H6	TLLVSTVQKRELVNP
44	D5	SYTSWFLDAFNAIL	92	H5	VSTVQKRELVNPASM
45	D4	SWFLDAFNAILKKI	93	H4	VQKRELVNPASMQQA
46	D3	LDAFNAILKKIDVL	94	H3	RELVNPASMQALIA
47	D2	FNYAILKKIDVLNLS	95	H2	VNPASMQALIASAR
48	D1	AILKKIDVLNLSIGG	96	H1	ASMKQALIASARRLP

FIG. 6B

97 I12 IKDFHVYFRESRDAG
98 I11 DAELHI FRVFTNNQV
99 I10 KQALIASARRLPGVN
100 I9 LIASARRLPGVNMFE
101 I8 SARRLPGVNMFEQGH
102 I7 RLPGVNMFEQGHGKL
103 I6 GVNMFEQGHGKLDLL
104 I5 MFEQGHGKLDLLRAY
105 I4 QGHGKLDLLRAYQIL
106 I3 GKLDLLRAYQILNSY
107 I2 DLLRAYQILNSYKPQ
108 I1 RAYQILNSYKPQASL
109 J12 QILNSYKPQASLSPS
110 J11 NSYKPQASLSPSYID
111 J10 KPQASLSPSYIDLTE
112 J9 ASLSPSYIDLTECPY
113 J8 SPSYIDLTECPYMWP
114 J7 YIDLTECPYMWPYCS
115 J6 LTECPYMWPYCSQPI
116 J5 CPYMWPYCSQPIYYG

FIG. 6C

0960
2000 1000 0
MKLVNIWLLLUVLLCGKKHLDRLLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFT
AKARNSFISSALKSSEVDNWRIIPRNNPSSDYPDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQR
KVFRSLKYAESDPTVPCNETRWSQWKQSSRPLRRASLSLGSFWHATGRHSSRLLRAI PRQVAQ
TLQADVLWQMGTGANVRVAVFDTGLSEKHFKNVKERTNWTNERLDDGLGHGTVAGVIASM
RECQGFAPDAELHI FRVFTNNQVSYTSWFLDAFNYA1LKKIDVLNLSIGGPDFMDHPFVDKVWEL
TANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMTTWELPGGYGRMKPD
IVTYGAGVRGSGVKGGCRALSGTVASPVVAGAVTLLVSTVQKRELVPASMKQALIASARLPG
VNMF EQHGKLDLLRAYQILNSYKPQASLSPSYIDLTECPYMWPYCSPQI YYGGMPTVVNTILN
GMGVTRIVDKPDWQPYLQNGDNIEVAFSYSSVLWPWSGYLAISISVTKAASWEGLAQGHVMI
TVASPAETESKNGAEQTSTVKLPIVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPL
DWNGDHHTNFRDYMQHLSRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRRDVD
NGLSLVIFSDWYNTSVMRKVFYDENTROWMPDTGGANI PALNELLSVWNMGFSDGLYEGEFTL
ANHDMDYYASGCSIAKFPEDGVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGRIVLYG
DSNCCLDDSHRQKDCFWLLDALLOYTSYGVTPPSLSHSGNRQPPSGAGSVTPERMGNHLHRYSK
VLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKVVLNPFRSNRPQVRPL
SPGESGAWDI PGIMPGRYNQEVGQTIPVFAFLGAMVVLAFFVVQINKAKSRPKRRKPRVKRPQL
MQQVHPPKTPSV

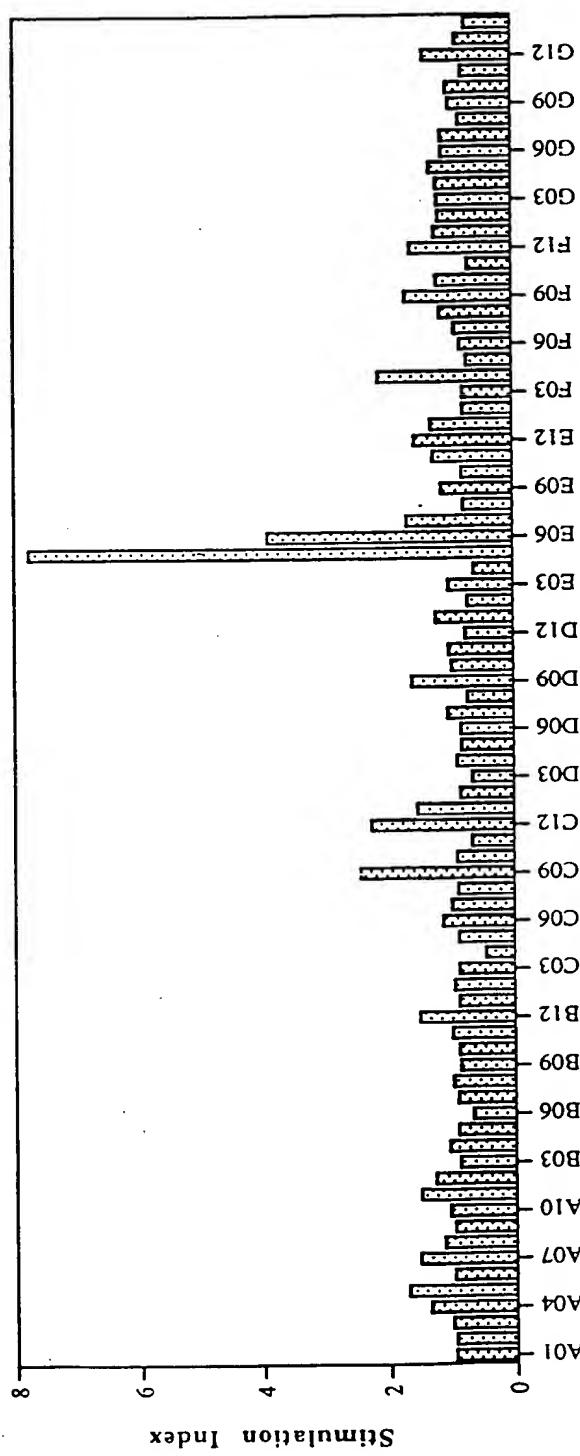
FIG. 7

	10	20	30	40	50
BPN	AQSVPYGVSQ - IKAPALHSQGYTGSNVKVAVIDSGIDSSHDLK - VAGGA				48
SAVINASE	AQSVPWGISR - VQAPAAHNRGLTGSGVKVALDGTI - STHPDLN - IRGGA				47
S2HSBT	- RAI PRQVAQTLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERT				49
	60	70	80	90	100
BPN	SMVPSETNPFPQDNNSHGTHVAGTVAAALNNSIGVLGVAPSASLYAVKVVLGA				98
SAVINASE	SFVPGEPST - QDGNGHGTHVAGTIAAALNNSIGVLGVAPSASELYAVKVVLGA				96
S2HSBT	NW - TNERTLDDGLGHGTFVAGVIASMRECQGF --- APDAELHIFRVFTN				94
	110	120	130	140	150
BPN	DGSGQYSWIINGIEWAIANNMDVINMSLGGPS - GSAALKAAVDKAVASGV				147
SAVINASE	SGSGSVSSIAQGLEWAGNNGMHVANLSLGSPS - PSATLEQAVNSATSRGV				145
S2HSBT	NQVSYTSWFLDASFNYAILKKIDVLNL SIGGPDFMDHPFVDKVWELTANNV				144
	160	170	180	190	200
BPN	VVVAAGNEGTSGSSTVGYPGKYPsviAVGAVDSSNQRASFSSVGPEL -				197
SAVINASE	LVVAASGNSGA --- GSISYPARYANAMAVGATDQNNNRASFSSQYGA GL -				191
S2HSBT	IMVSAIGNDGP -- LYGTLN PADQMDVIGVGGIDFEDNIARFSSRGMTTW				192
	210	220	230	240	250
BPN	----- DVMAPGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALIL				235
SAVINASE	----- DIVAPGVNVQSTYPGSTYASLNGTSMATPHVAGAAALVK				229
S2HSBT	ELPGGYGRMKPDIVTYGAGVRGSGVKGGCRALSGTSVASPVVAGVTLLV				242
	260	270	280	290	
BPN	SKHPNWTNTQ --- VRSSLENTTTKLGDsfYYGKGLINVQAAAQ				275
SAVINASE	QKNPSWSNVQ --- IRNHLKNTATSLGSTNLYGSGLVNAEAATR				269
S2HSBT	STVQKRELVNPA SMKQALIASARRLPGVNMFEQG --- HGKL				280

FIG. 8

Well Position

FIG. 9



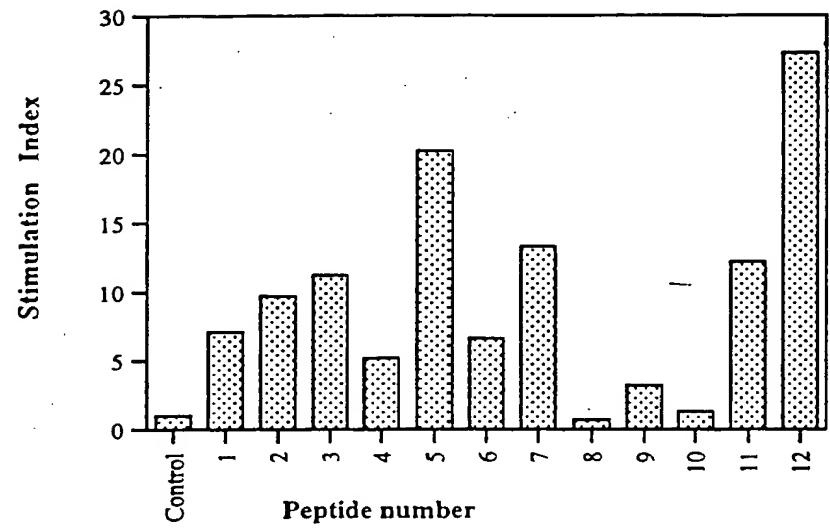
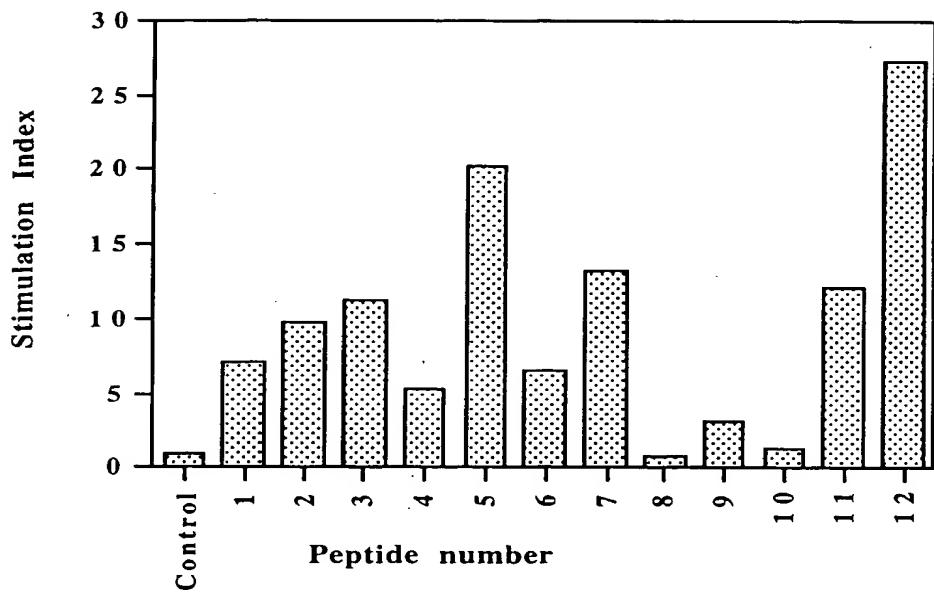


FIG. 10



Peptide number	Sequence
1 (unmodified sequence)	GSISYPARYANAMAV
2	ASISYPARYANAMAV
3	GAISYPARYANAMAV
4	GSASYPARYANAMAV
5	GSIAYPARYANAMAV
6	GSISAPARYANAMAV
7	GSISYAARYANAMAV
8	GSISYPAAYANAMAV
9	GSISYPARAANAMAV
10	GSISYPARYAAAMAV
11	GSISYPARYANAAAV
12	GSISYPARYANAMAA

FIG. 11

Human subtilisin percent responders

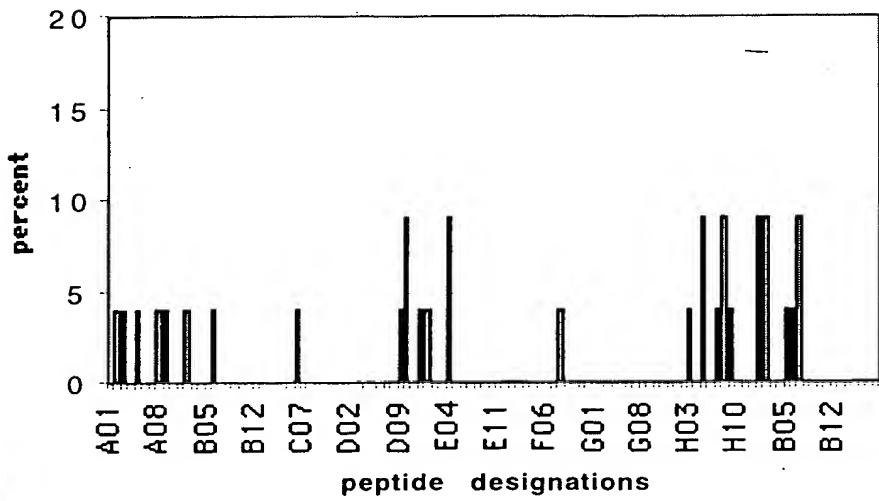


FIG. 12

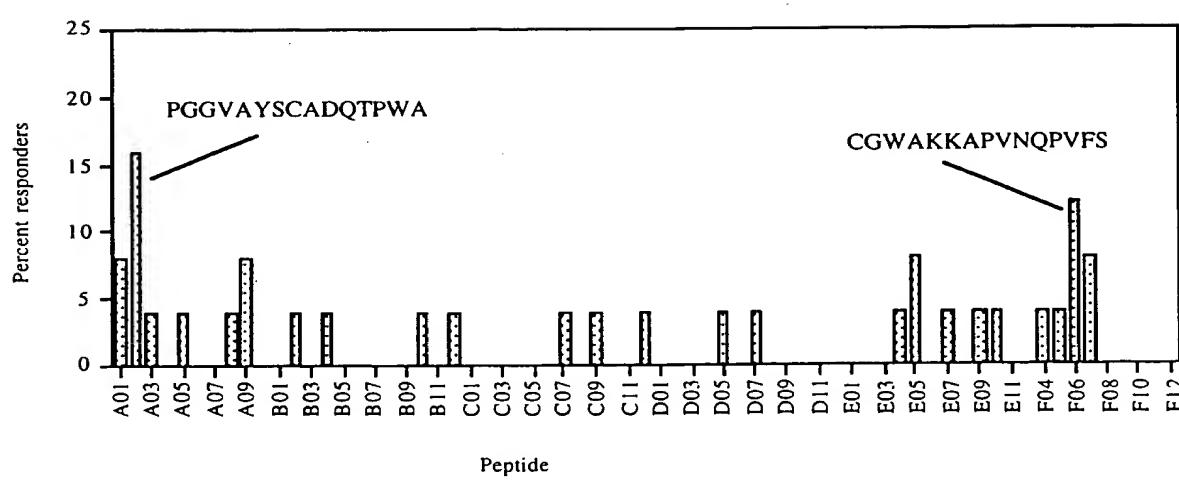


FIG. 13A

9
8
7
6
5
4
3
2
1

1	2	3	4	5
1234567890	1234567890	1234567890	1234567890	1234567890
MRSSPLLPSA	VVAALPVIAL	AADGRSTRYW	<u>DCCKPSCGWA</u>	<u>KKAPVNQPVF</u>
<u>SCNANFQRIT</u>	<u>DFDAKSGCEP</u>	<u>GGVAYSCADQ</u>	<u>TPWAVNDDFA</u>	LGFAATSIAG
SNEAGWCCAC	YELTFTSGPV	AGKKMVVQST	STGGDLGSNH	FDLNIPGGGV
GIFDGCTPQF	GGLPGQRYGG	ISSRNECDRF	PDALKPGCYW	RFDWFKNADN
PSFSFRQVQC	PAELVARTGC	RRNDDGNFPA	VQIPSSSTSS	PVNQPTSTST
TSTSTTSSPP	VQPTTPSGCT	AERWAQ		

FIG. 13B

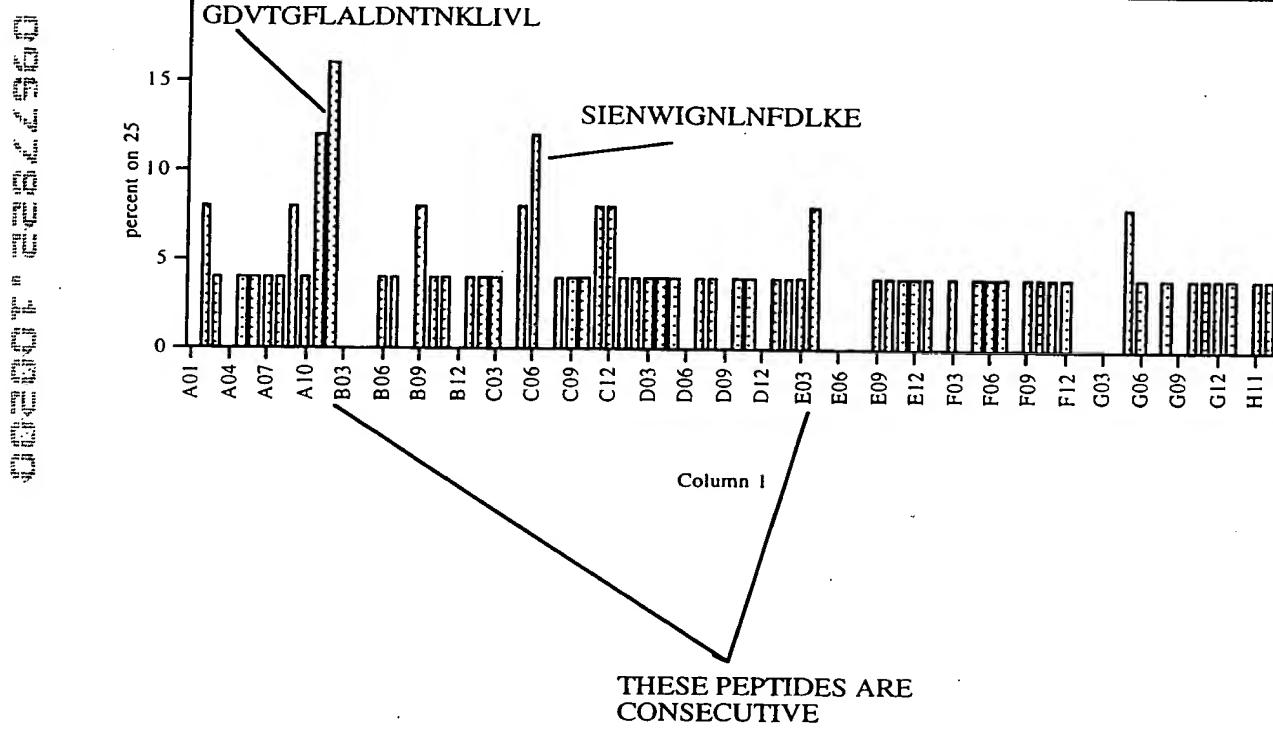


FIG. 14A

1 mrsslvlfv sawtalaspi rrevsqdlfn qfnlfaqysa aaycgknnda
51 pagtnitctg nacpevekad atflysfeds **gvqdvtqfla ldntnklivl**
101 sfrgsrsien **wignlnfdlk** eindicsgcr ghdgftsswr svadtlrqkv
151 edavrehpdy rvvftghs1g galatvagad lrgngydidv fsygaprvgn
201 rafaefltvq tgglyrith tndivprlpp refgyshssp eywiksgtlv
251 pptrndivki egidatggnn qpnipdipah lwyfgligtc 1

FIG. 14B

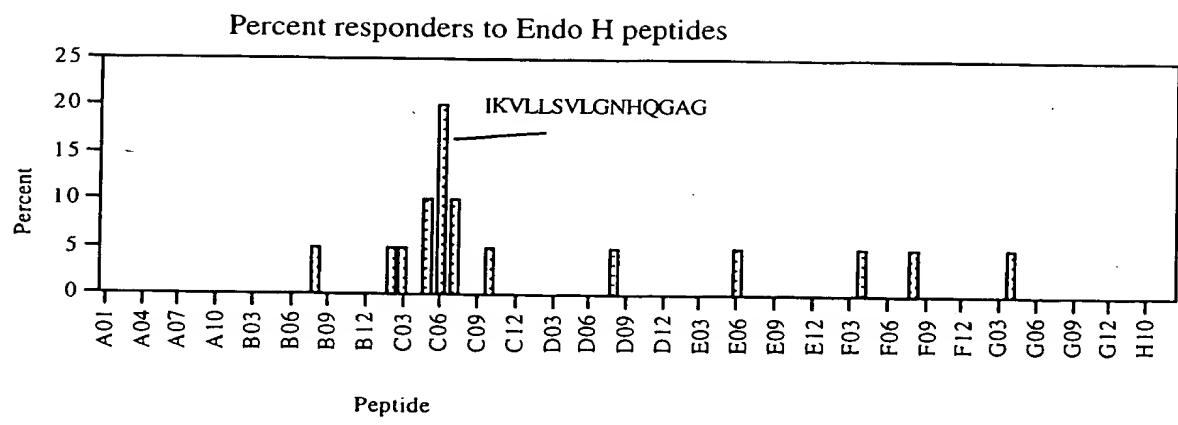


FIG. 15A

1 mftpvrrrvr taalalsaaa alvlgstaas gasatpspap apapapkqg
51 ptsvayvevn nnsmlnvkky tladgggnaf dvavifaani nydtgtktay
101 lhfnenvqrv ldnavtqirp lqqqgik**v**ll s**v**lqnqaq fanfpsqaa
151 safakqlsda vakygldgvd fddeyaeygn ngtaqpdss fvhltalra
201 nmpdkiisly nigpaasrls yggvdvsdkf dyawnpyygt wqvpgialpk
251 aqlspaavei grtsrstvad larrtvdegy gvyltnldg gdrtadvsaf
301 trelygseav rtp

FIG. 15B

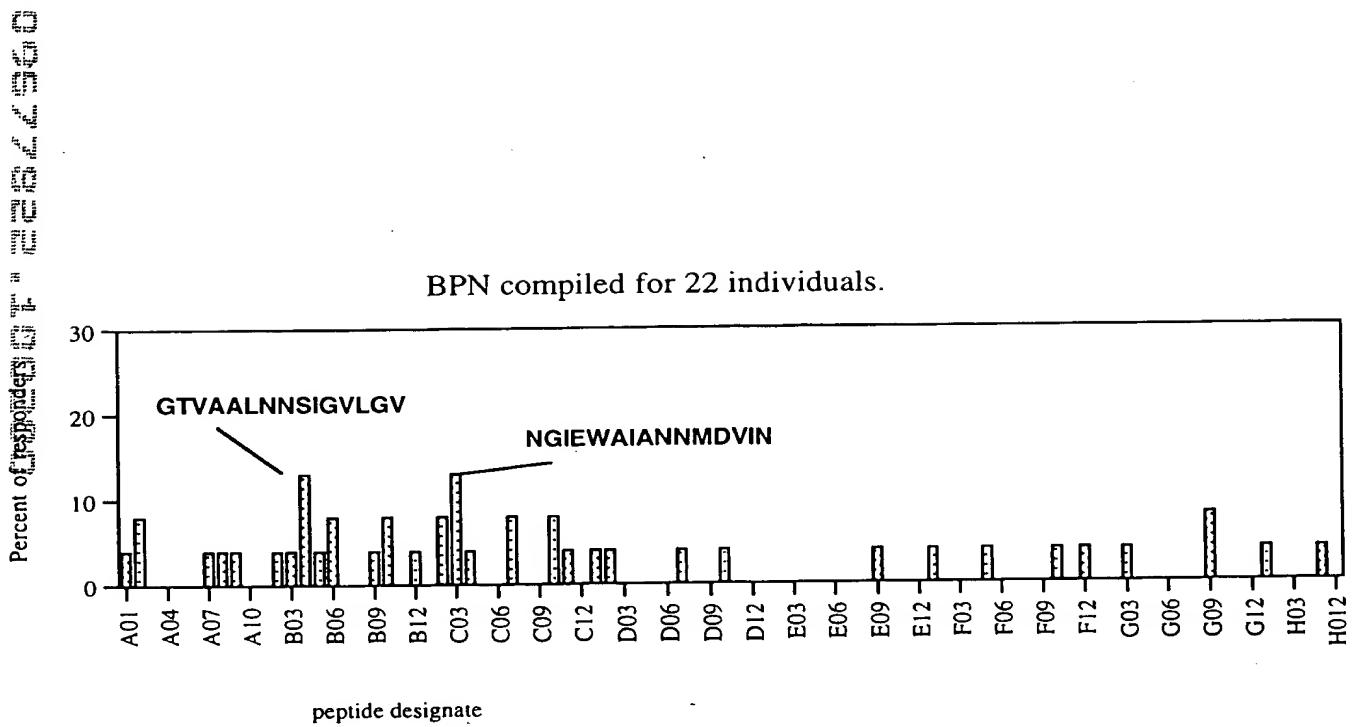


FIG. 16

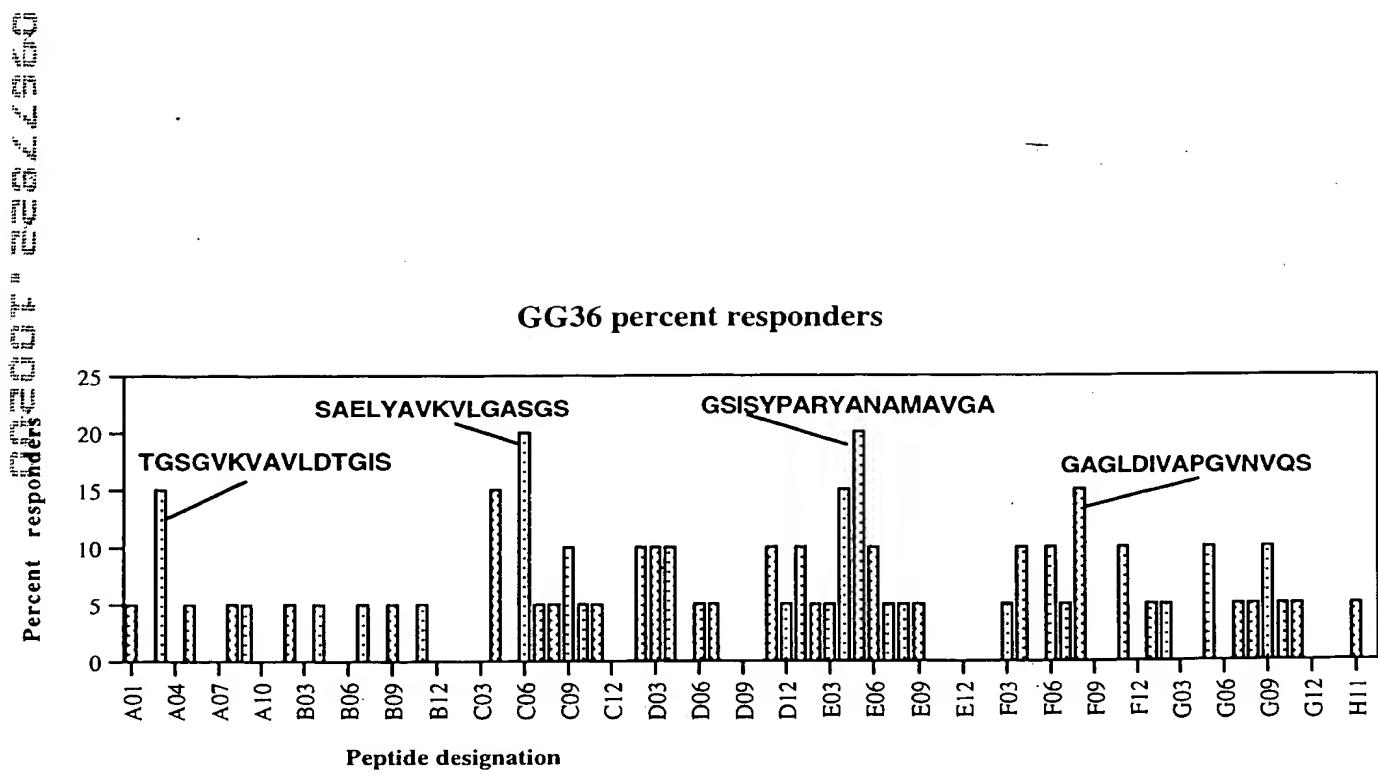


FIG. 17

Hybrid enzyme sequence (GG36-BPN)

GG36

AQSVPWGISRVQAPAAHNRLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEpstQDGNGH

BPN

GTHVAGTIAALNNSIGVLGVAPS AELYAVKVL GAS GSG VSSIA QGLE WAG NNG MHV INMSL GG S

△

GSAALKAAVDKAVASGVVVVAAAGNEGTGS S STVGYPGK YPSVIAVGAVDSSNQRASFSSVGP

ELDVMAPGVSIQSTLPGNKYGA YNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTKLG D

SFYY GKGLINVQAAAQ

FIG. 18

00000000000000000000000

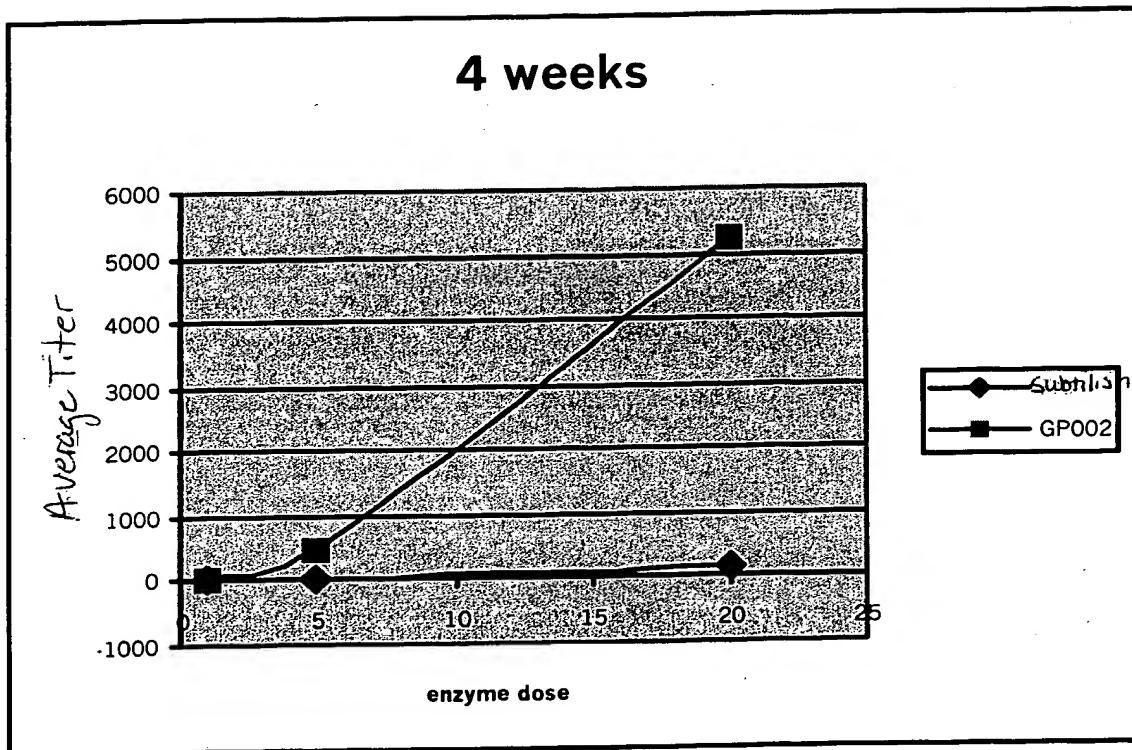


FIGURE 19A

300200312200300

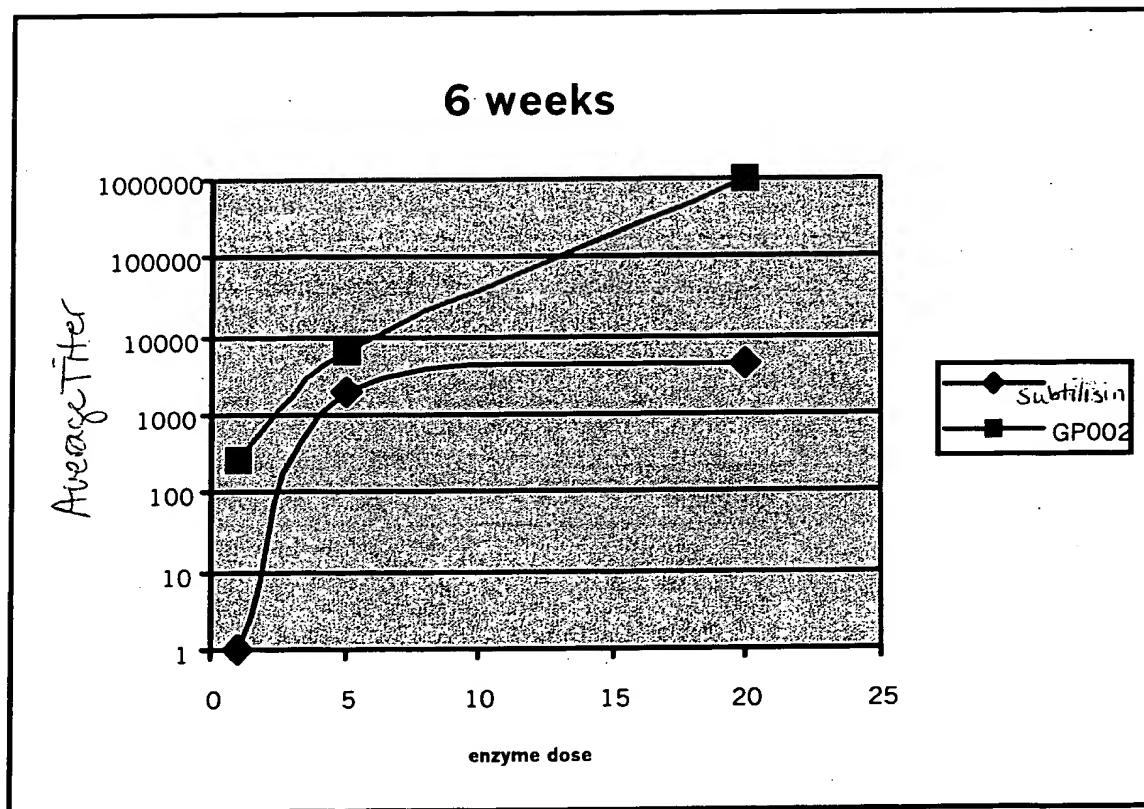


FIGURE 19B

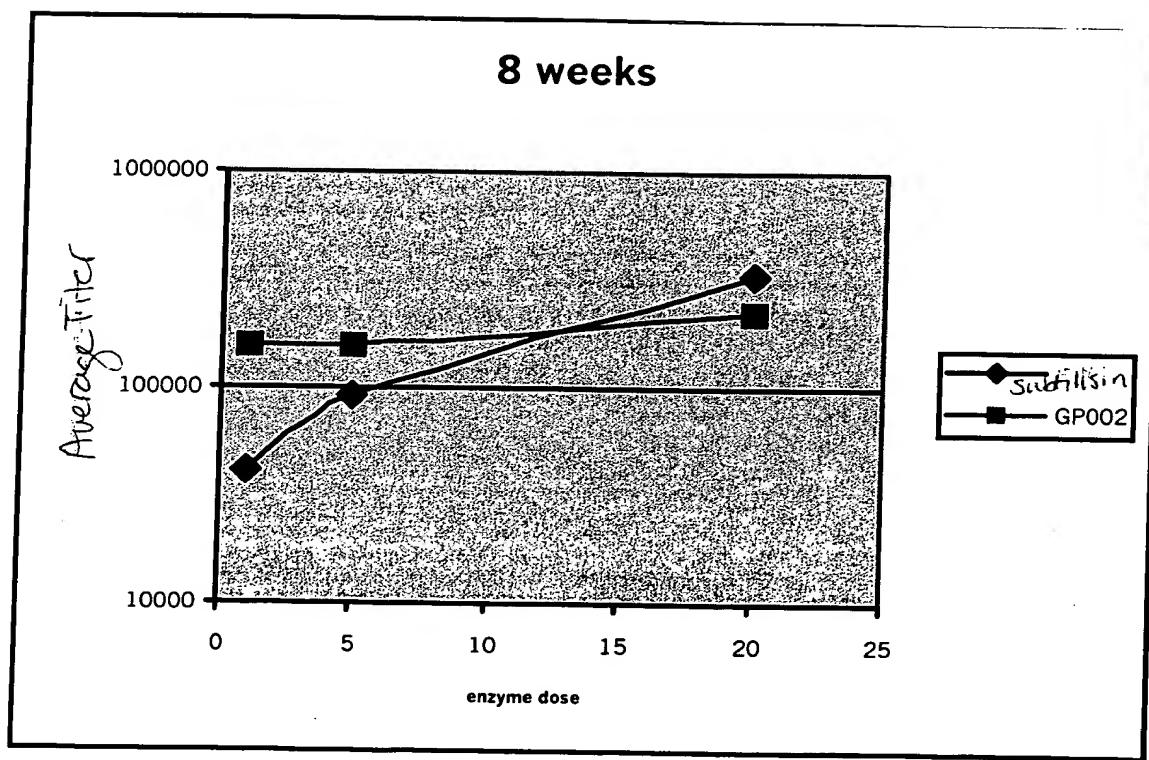


FIGURE 19C

Figure 19D

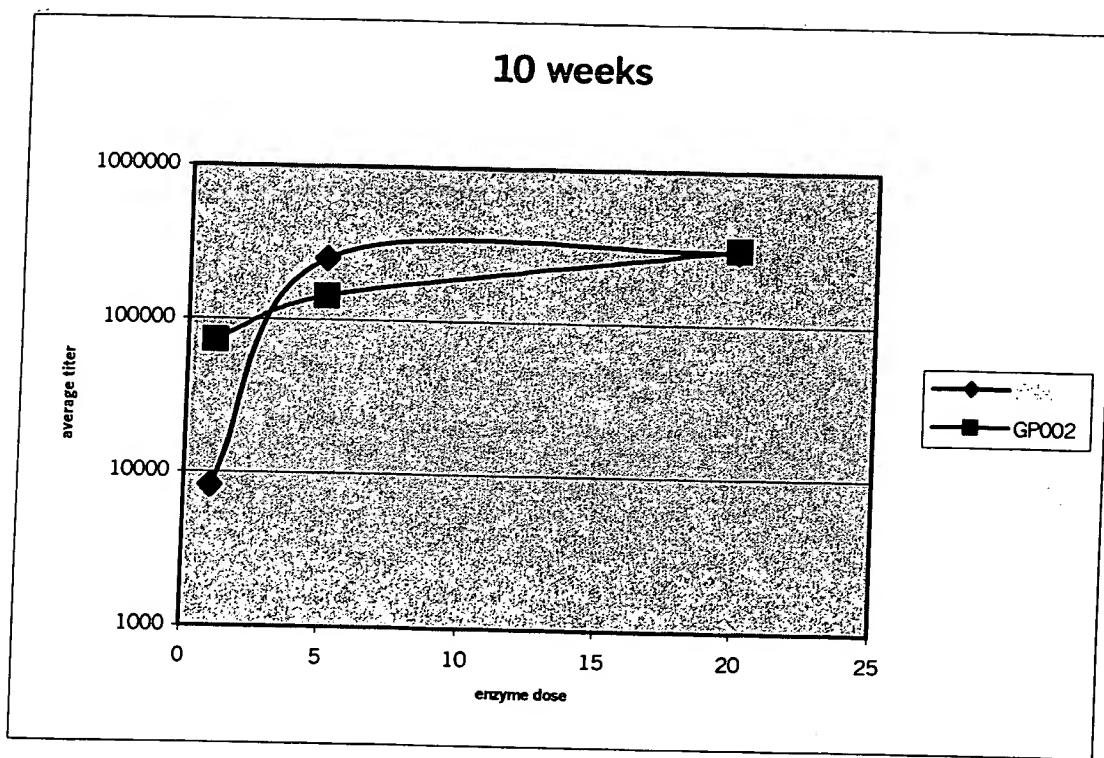


FIGURE 19D

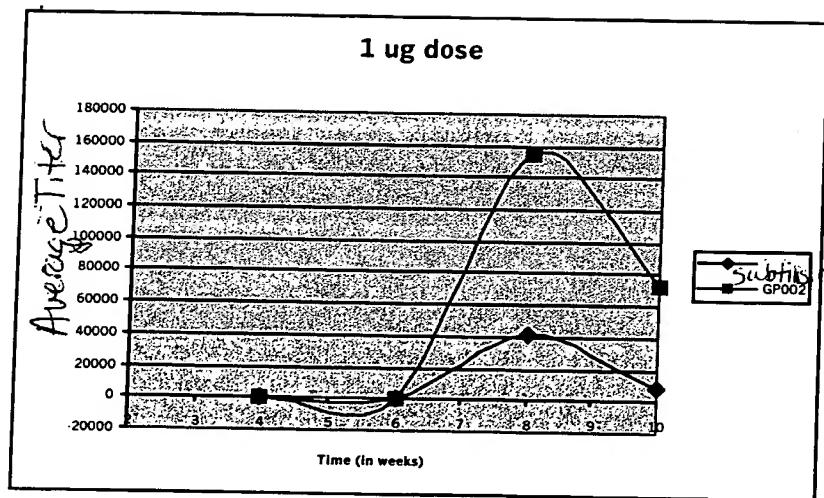


FIGURE 20A

20202020202020202020

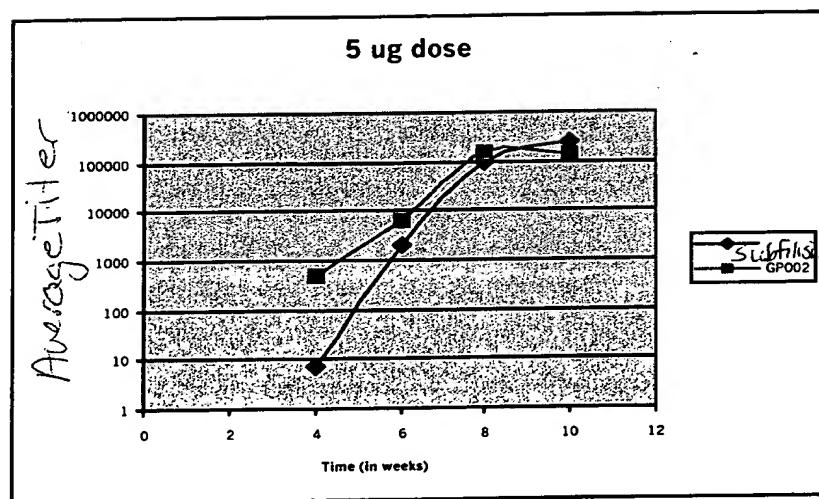


FIGURE 20B

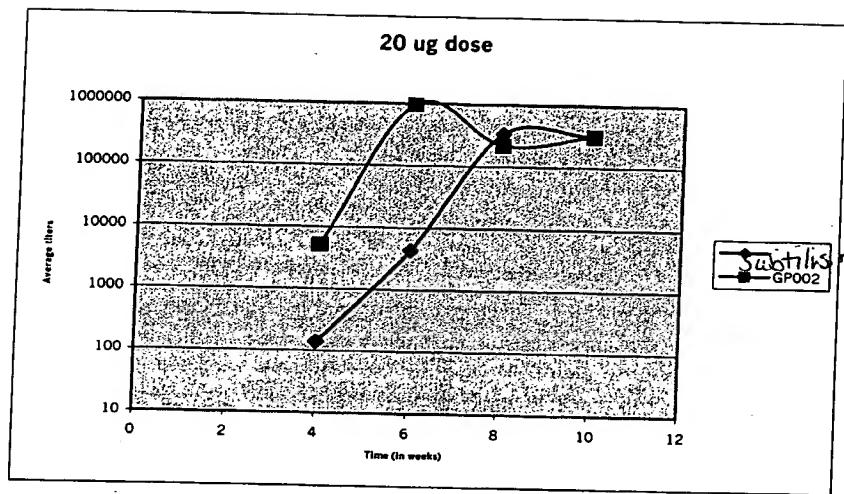


FIGURE 20C